

Class 7: Machine Learning 1

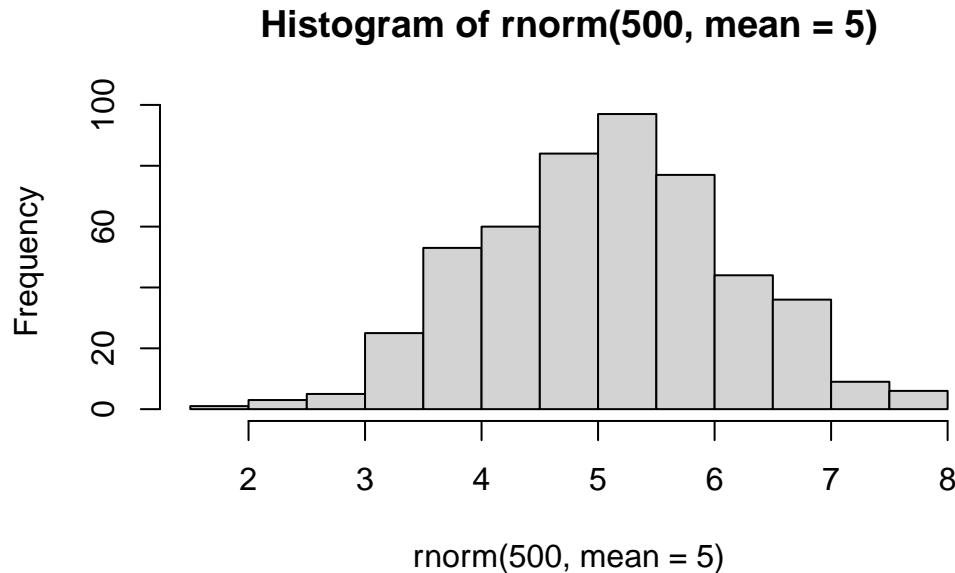
Junlin Ruan (PID: A17839687)

Today we will explore some fundamental machine learning methods including clustering and dimensionality reduction.

K-means clustering

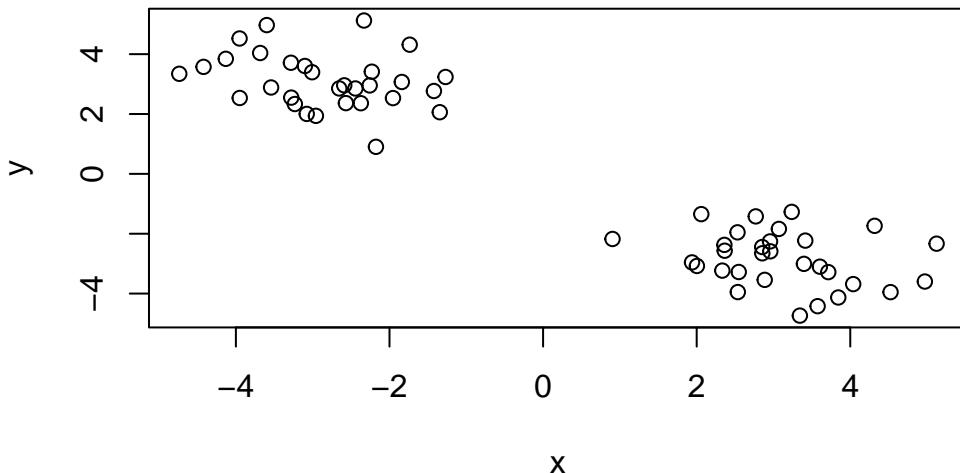
To see how this works let's first makeup some data to cluster where we know the answer should be. We can use the `rnorm()` function to help here:

```
hist(rnorm(500, mean = 5))
```



```
x <- c(rnorm(30, mean=-3), rnorm(30, mean=3))  
y <- rev(x)
```

```
x <- cbind(x,y)  
plot(x)
```



The function for K-means clustering in “base” R is `kmeans()`

```
k <- kmeans(x, centers = 2)  
k
```

K-means clustering with 2 clusters of sizes 30, 30

Cluster means:

	x	y
1	-2.838178	3.101070
2	3.101070	-2.838178

Clustering vector:

```
Within cluster sum of squares by cluster:  
[1] 49.44771 49.44771  
  (between_SS / total_SS =  91.5 %)
```

Available components:

```
[1] "cluster"      "centers"       "totss"        "withinss"      "tot.withinss"  
[6] "betweenss"    "size"          "iter"         "ifault"
```

To get at the results of the returned list object we can use the dollar \$ syntax

Q. How many points are in each cluster?

k\$size

[1] 30 30

Q. What ‘component’ of your result object details - cluster assignment/membership? - cluster center?

k\$cluster

k\$centers

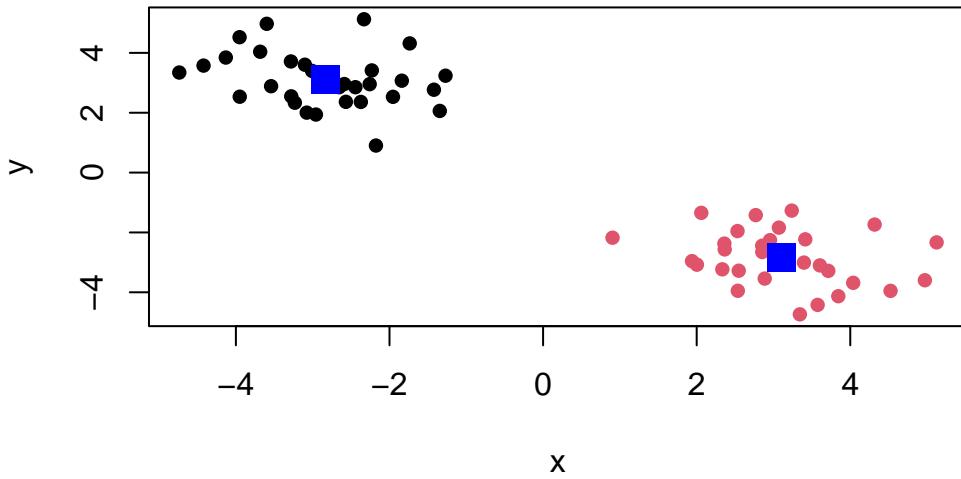
```

          x           y
1 -2.838178  3.101070
2  3.101070 -2.838178

```

Q. Make a clustering results figure of the data colored by cluster membership and show cluster centers.

```
plot(x, col = k$cluster, pch = 16)
points(k$centers, col = "blue", pch = 15, cex = 2)
```

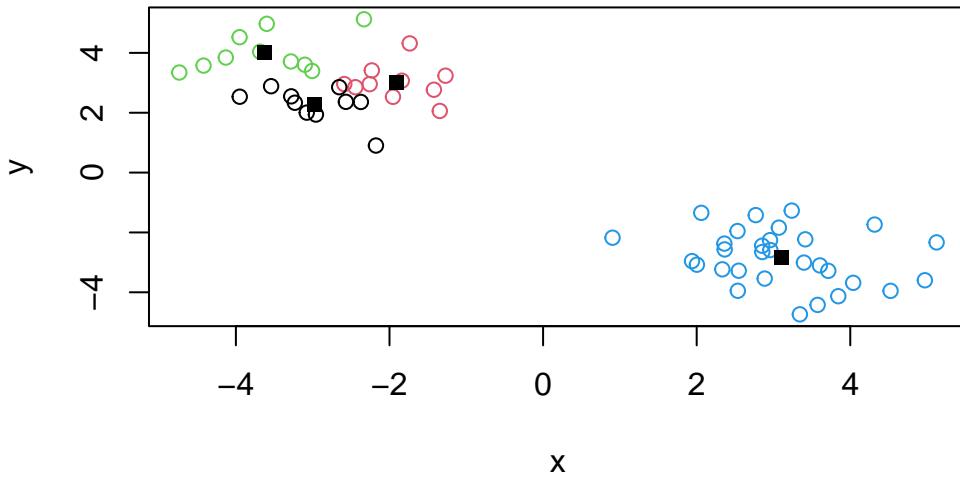


K-means clustering is very popular as it is very fast and relatively straight forward: it takes numeric data as input and returns the cluster membership vector etc.

The “issue” is we tell `kmeans()` how many clusters we want!

Q. Run kmeans again and cluster into 4 groups/clusters and plot results like we did above.

```
k4 <- kmeans(x, centers = 4)
plot(x, col = k4$cluster)
points(k4$centers, pch = 15)
```

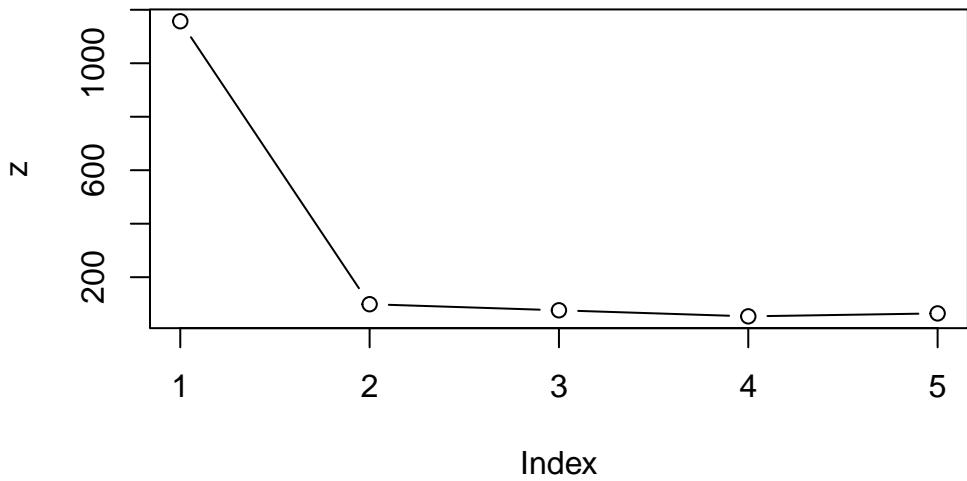


Scree plot to pick k centers value

brute-force

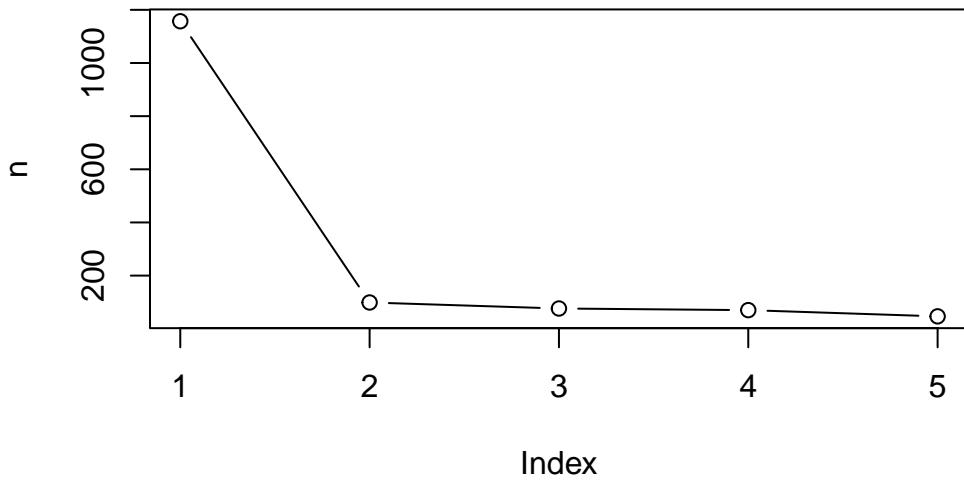
```
k1 <- kmeans(x, centers = 1)
k2 <- kmeans(x, centers = 2)
k3 <- kmeans(x, centers = 3)
k4 <- kmeans(x, centers = 4)
k5 <- kmeans(x, centers = 5)
```

```
z <- c(k1$tot.withinss,
       k2$tot.withinss,
       k3$tot.withinss,
       k4$tot.withinss,
       k5$tot.withinss)
plot(z, typ="b")
```



```
n <- NULL
for(i in 1:5){
  n <- c(n, kmeans(x, center = i)$tot.withinss)
}

plot(n, typ = "b")
```



Hierarchical Clustering

The main “base” R function for Hierarchical Clustering is called `hclust()`. Here we can’t just input our data we need to first calculate a distance matrix (e.g. `dist()`) for our data and use this as input to `hclust()`.

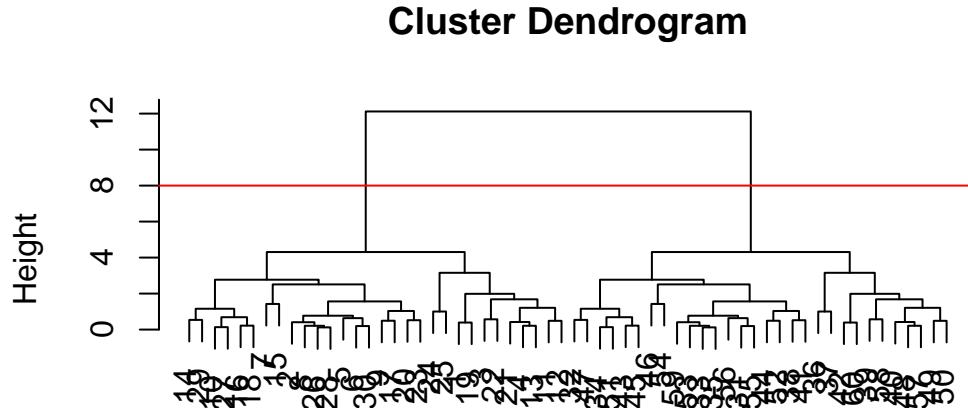
```
d <- dist(x)
hc <- hclust(d)
hc
```

```
Call:
hclust(d = d)
```

```
Cluster method : complete
Distance       : euclidean
Number of objects: 60
```

There is a plot method for `hclust` results lets try it

```
plot(hc)
abline(h = 8, col = "red")
```



```
d  
hclust (*, "complete")
```

To get our cluster “membership” vector (i.e. our main clustering result) we can “cut” the tree at a given height or at a height that yields a given “ k ” groups.

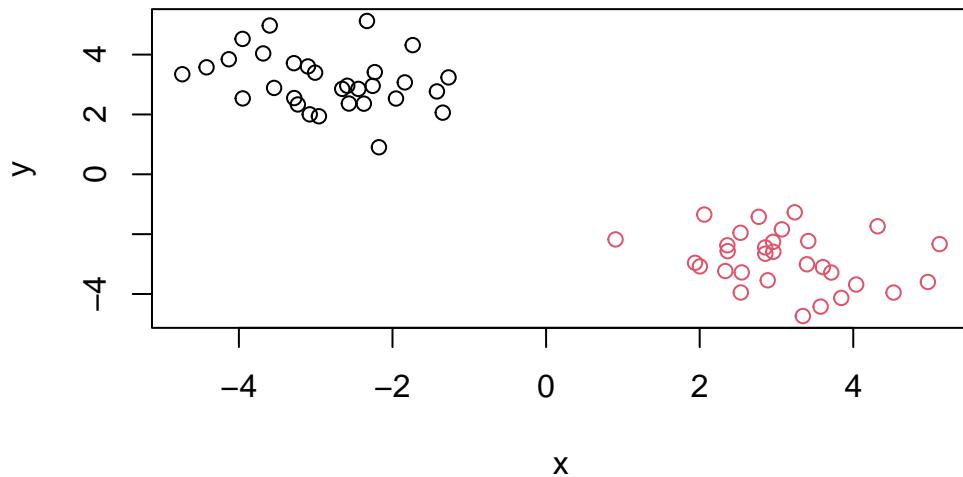
```
cutree(hc, h = 8)
```

```
cutree(hc, k = 2)
```

```
grps <- cutree(hc, k=2)
```

Q. Plot the data with out hclust result coloring

```
plot(x, col = grps)
```



Principal Component Analysis (PCA)

PCA of UK food data

Import food data from an online CSV file.

```
url <- "https://tinyurl.com/UK-foods"  
x <- read.csv(url)  
head(x)
```

		X	England	Wales	Scotland	N.Ireland
1	Cheese		105	103	103	66
2	Carcass_meat		245	227	242	267
3	Other_meat		685	803	750	586
4	Fish		147	160	122	93
5	Fats_and_oils		193	235	184	209
6	Sugars		156	175	147	139

```

rownames(x) <- x[,1]
x <- x[ , -1]
x

```

	England	Wales	Scotland	N.Ireland
Cheese	105	103	103	66
Carcass_meat	245	227	242	267
Other_meat	685	803	750	586
Fish	147	160	122	93
Fats_and_oils	193	235	184	209
Sugars	156	175	147	139
Fresh_potatoes	720	874	566	1033
Fresh_Veg	253	265	171	143
Other_Veg	488	570	418	355
Processed_potatoes	198	203	220	187
Processed_Veg	360	365	337	334
Fresh_fruit	1102	1137	957	674
Cereals	1472	1582	1462	1494
Beverages	57	73	53	47
Soft_drinks	1374	1256	1572	1506
Alcoholic_drinks	375	475	458	135
Confectionery	54	64	62	41

```

x <- read.csv(url, row.names = 1)
x

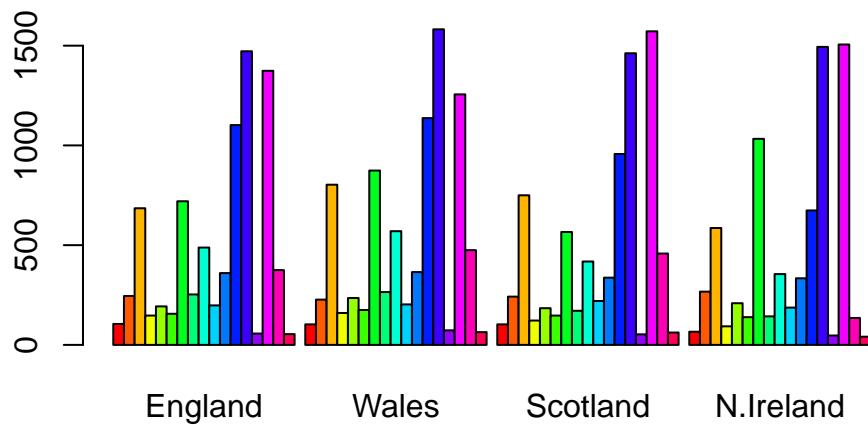
```

	England	Wales	Scotland	N.Ireland
Cheese	105	103	103	66
Carcass_meat	245	227	242	267
Other_meat	685	803	750	586
Fish	147	160	122	93
Fats_and_oils	193	235	184	209
Sugars	156	175	147	139
Fresh_potatoes	720	874	566	1033
Fresh_Veg	253	265	171	143
Other_Veg	488	570	418	355
Processed_potatoes	198	203	220	187
Processed_Veg	360	365	337	334
Fresh_fruit	1102	1137	957	674
Cereals	1472	1582	1462	1494
Beverages	57	73	53	47

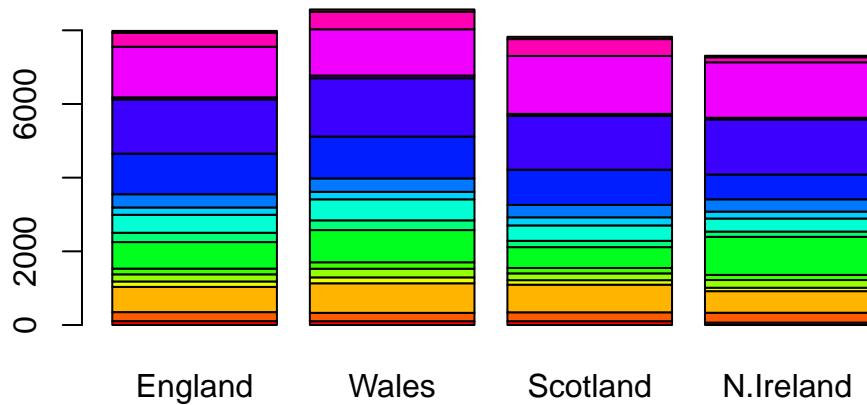
Soft_drinks	1374	1256	1572	1506
Alcoholic_drinks	375	475	458	135
Confectionery	54	64	62	41

Some base figures

```
barplot(as.matrix(x), beside=T, col=rainbow(nrow(x)))
```

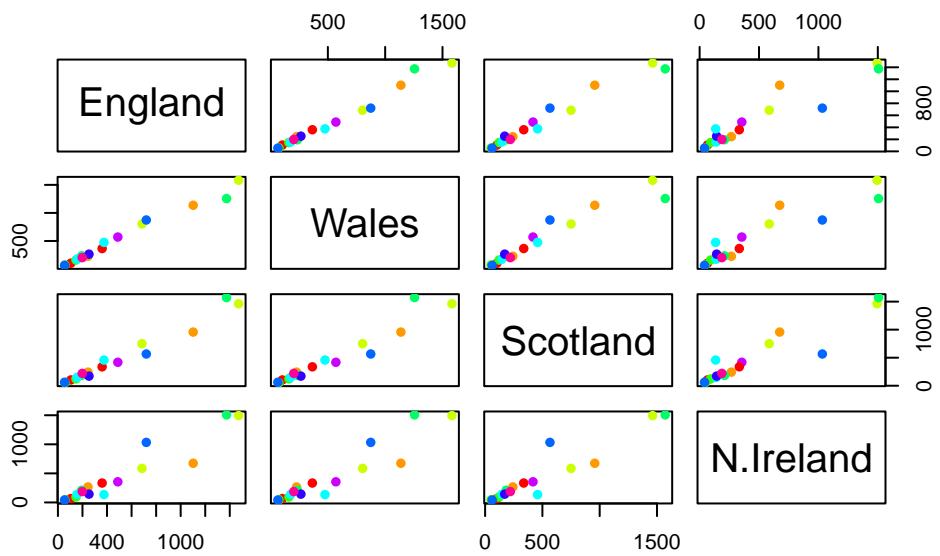


```
barplot(as.matrix(x), col=rainbow(nrow(x)))
```



There is one plot that can be useful for small datasets:

```
pairs(x, col=rainbow(10), pch=16)
```



Main point: It can be difficult to spot major trends and patterns even in relatively small multivariate dataset (here we only have 17 dimensions, typically we have 1000s).

```
#PCA to the rescue
```

The main function in “base” R for PCA is called `prcomp()`

I will take the transpose of our food data so the “foods” are in the columns:

```
pca <- prcomp(t(x))
summary(pca)
```

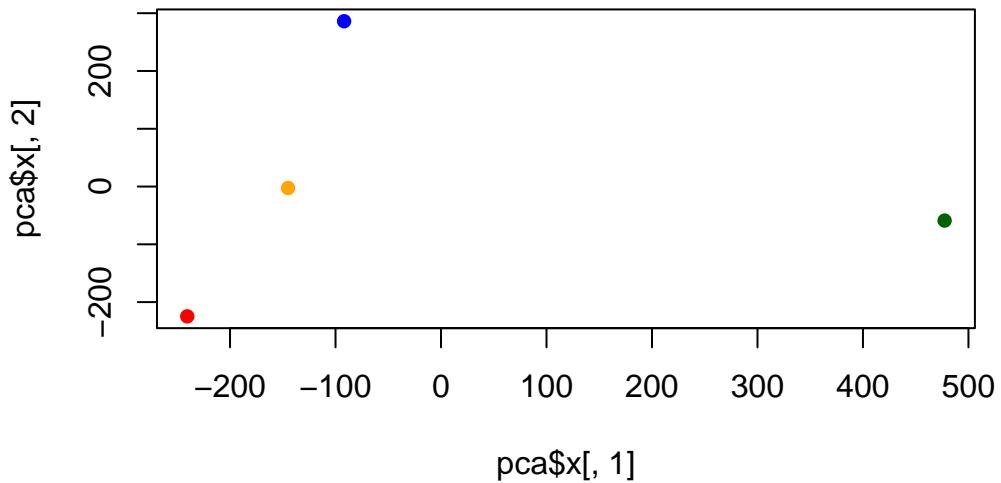
Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	324.1502	212.7478	73.87622	2.921e-14
Proportion of Variance	0.6744	0.2905	0.03503	0.000e+00
Cumulative Proportion	0.6744	0.9650	1.00000	1.000e+00

```
pca$x
```

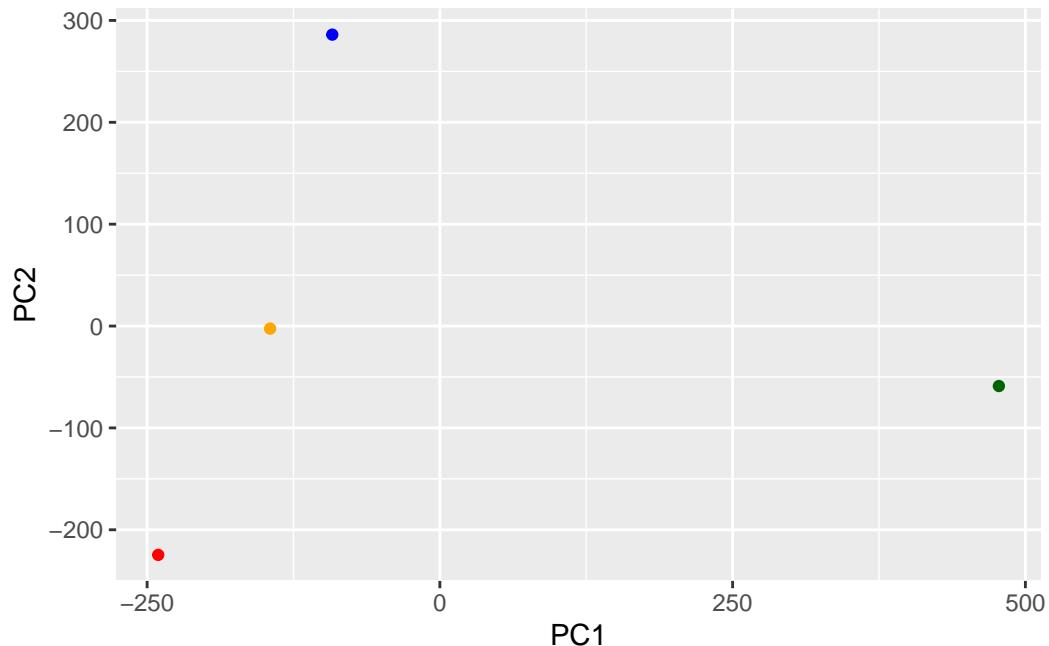
	PC1	PC2	PC3	PC4
England	-144.99315	-2.532999	105.768945	-9.152022e-15
Wales	-240.52915	-224.646925	-56.475555	5.560040e-13
Scotland	-91.86934	286.081786	-44.415495	-6.638419e-13
N.Ireland	477.39164	-58.901862	-4.877895	1.329771e-13

```
cols <- c("orange","red","blue","darkgreen")
plot(pca$x[,1], pca$x[,2], col = cols, pch = 16)
```

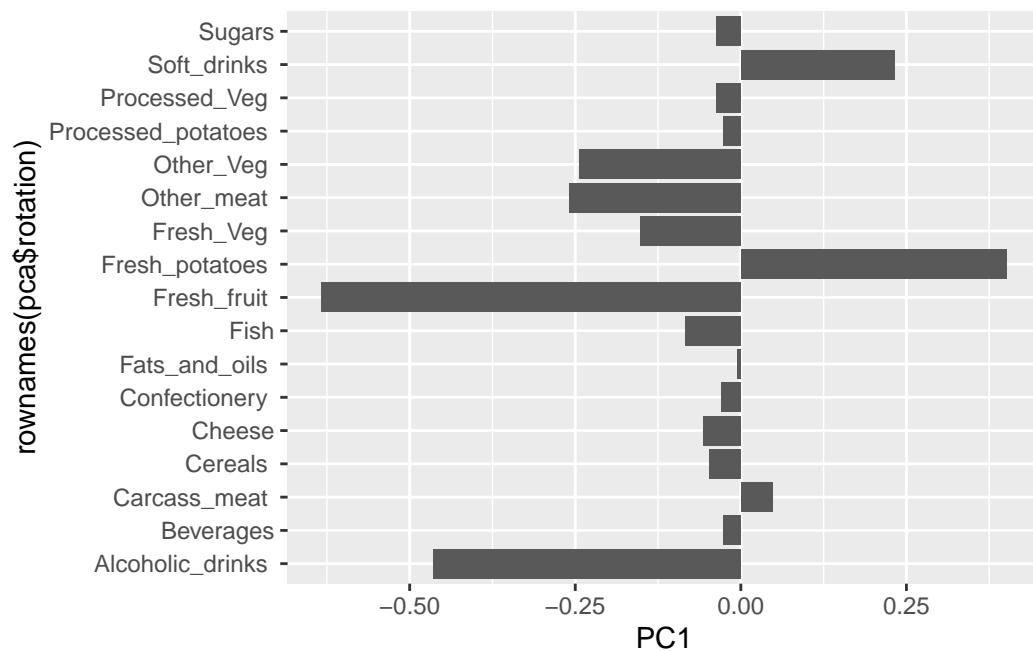


```
library(ggplot2)

ggplot(pca$x) +
  aes(PC1,PC2) +
  geom_point(col = cols)
```



```
ggplot(pca$rotation) +
  aes(PC1, rownames(pca$rotation)) +
  geom_col()
```



PCA looks super useful and we will come back to describe this further next day :-)